

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 2, 2002, 01:30:59 ; Search time 85.5728 Seconds  
(without alignments)  
6074.559 Million cell updates/sec

Title: us-09-856-979-6

Perfect score: 1695  
Sequence: 1 ccgcagctctctgtgtga.....tccatcaagccgtgcgatg 1695

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued\_Patents\_NA: \*  
1: /cgn2.6/ptodata/1/ina/5A.COMB.seq: \*  
2: /cgn2.6/ptodata/1/ina/5B.COMB.seq: \*  
3: /cgn2.6/ptodata/1/ina/6A.COMB.seq: \*  
4: /cgn2.6/ptodata/1/ina/6B.COMB.seq: \*  
5: /cgn2.6/ptodata/1/ina/PCTUS.COMB.seq: \*  
6: /cgn2.6/ptodata/1/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1695	100.0	5349	4	US-09-068-101-7
2	1695	100.0	6548	3	US-08-817-188-2
3	1693.4	99.9	2407	1	US-08-104-072B-8
4	1693.4	99.9	2407	1	US-08-351-413-9
5	1693.4	99.9	2407	2	US-09-025-583-9
6	1693.4	99.9	6548	3	US-08-894-440-1
7	1693.4	99.9	6548	4	US-09-458-093-1
8	37.6	2.2	3033	1	US-09-134-001C-2341
9	36.6	2.2	7218	1	US-08-232-463-14
10	35.6	2.1	29793	4	US-09-302-812-38
11	35.6	2.1	29793	4	US-09-511-477-38
12	35.6	2.1	29793	4	US-09-511-507-38
13	35.2	2.1	1831	6	5215881-1
14	35.2	2.1	1831	6	5215881-3
15	34.2	2.0	8050	4	US-09-491-362-11
16	34.2	2.0	8050	4	US-09-874-562-11
17	34	2.0	888	4	US-09-134-001C-1629
18	34	2.0	169998	4	US-09-676-610B-24
19	33.8	2.0	4084	3	US-08-866-340-1
20	33.8	2.0	4460	4	US-09-103-875-4
21	33.6	2.0	1715	2	US-08-467-963C-26
22	33.6	2.0	1715	2	US-08-838-189D-26
23	33.6	2.0	1715	3	US-08-852-344D-26
24	33.6	2.0	1715	3	US-08-344-639E-26
25	33.6	2.0	1833	2	US-08-467-963C-3
26	33.6	2.0	1833	2	US-08-838-189D-3
27	33.6	2.0	1833	3	US-08-852-344D-3

28	33.6	2.0	1833	3	US-08-344-639E-3	Sequence 3, Appli
29	33.6	2.0	1833	4	US-08-467-969A-3	Sequence 3, Appli
30	33.6	2.0	1833	4	US-08-467-961A-3	Sequence 3, Appli
31	33.6	2.0	1833	4	US-08-001-554A-3	Sequence 3, Appli
32	33.6	2.0	1856	2	US-08-360-606B-29	Sequence 29, Appli
33	33.6	2.0	2935	4	US-09-480-921B-27	Sequence 27, Appli
34	33.4	2.0	2936	4	US-09-166-350-6	Sequence 6, Appli
35	33.2	2.0	1197	2	US-08-829-026A-5	Sequence 5, Appli
36	32.6	1.9	9060	4	US-08-378-313-20	Sequence 20, Appli
37	32.2	1.9	4161	3	US-08-790-517-1	Sequence 1, Appli
38	32.2	1.9	4161	3	US-08-790-517-1	Sequence 1, Appli
39	32	1.9	1719	3	US-08-987-439-4	Sequence 4, Appli
40	31.8	1.9	1038	1	US-08-134-570-13	Sequence 13, Appli
41	31.8	1.9	1226	4	US-09-276-593-3	Sequence 3, Appli
42	31.8	1.9	2064	4	US-09-276-599-2	Sequence 2, Appli
43	31.8	1.9	2763	4	US-09-489-868A-3	Sequence 3, Appli
44	31.8	1.9	3083	4	US-09-276-599-1	Sequence 1, Appli
45	31.8	1.9	6202	1	US-08-484-101B-41	Sequence 41, Appli

#### ALIGNMENTS

RESULT 1  
US-09-068-101-7  
; Sequence 7, Application US/09068101  
; Patent No. 6372960  
; GENERAL INFORMATION:  
; APPLICANT: PLANT GENETIC SYSTEMS N.V.  
; TITLE OF INVENTION: Improved Barstar Gene  
; FILE REFERENCE: 2121-139P  
; CURRENT APPLICATION NUMBER: US/09/068,101  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: EP 96202446.9  
; EARLIER FILING DATE: 1996-09-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 5349  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: other nucleic  
; OTHER INFORMATION: acid, "T-DNA of pTTS243"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: Complement(1)..(25))  
; OTHER INFORMATION: label = RB, "T-DNA right border"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: Complement(98)..(331))  
; OTHER INFORMATION: label = 3'g7, "region containing 3' untranslated  
; OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: Complement((332)..(883))  
; OTHER INFORMATION: label = bar, "region coding for phosphinethricin  
; OTHER INFORMATION: acetyl transferase"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: Complement((884)..(2258))  
; OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic  
; OTHER INFORMATION: Virus"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2281)..(3969)  
; OTHER INFORMATION: label = PEI, "promoter of El gene of rice (WO  
; OTHER INFORMATION: 92/13956)"  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (3970)..(4245)  
; OTHER INFORMATION: label = synb\*, "improved barstar DNA"  
; FEATURE:



SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 6548

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: plasmid pTS172

FEATURE:

NAME/KEY: misc\_feature

LOCATION: Complement((2019)..(2288))

OTHER INFORMATION: 3' nos: 3' untranslated region containing the

OTHER INFORMATION: polyadenylation signal of the nopaline synthase

OTHER INFORMATION: gene of Agrobacterium T-DNA.

FEATURE:

NAME/KEY: misc\_feature

LOCATION: Complement((2289)..(2624))

OTHER INFORMATION: Barnase: region coding for barnase

FEATURE:

NAME/KEY: misc\_feature

LOCATION: Complement((2625)..(4313))

OTHER INFORMATION: PEL: promoter region of E1 gene of rice

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (4336)..(5170)

OTHER INFORMATION: P35S: 35S promoter region of Cauliflower Mosaic

OTHER INFORMATION: Virus

FEATURE:

NAME/KEY: misc\_feature

LOCATION: Complement((5711)..(6262))

OTHER INFORMATION: bar: region coding for phosphinotricin

OTHER INFORMATION: acetyltransferase

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (6263)..(6496)

OTHER INFORMATION: 3' g7: 3' untranslated region containing the

OTHER INFORMATION: polyadenylation signal of gene 7 of Agrobacterium

OTHER INFORMATION: T-DNA

US-08-817-188-2

Query Match

Best Local Similarity 100.0%; Score 1695; DB 3; Length 6548;

Mismatches 0; Gaps 0;

Mismatches 1695; Conservative 0; Indels 0; Gaps 0;

QY 1 CGCGAGATCCCTCTGCTGATGTTTTATTAATAATTTATCTCGAATACCTACC 60

|||||

Db 4316 CGCGAGATCCCTCTGCTGATGTTTTATTAATAATTTATCTCGAATACCTACC 4257

|||||

QY 61 AATATATAGTAGACTTCTCAAGCTGCAAGAACTTCCAATCGCGACAATACCATAGAGA 120

|||||

Db 4256 AATATATAGTAGACTTCTCAAGCTGCAAGAACTTCCAATCGCGACAATACCATAGAGA 4197

|||||

QY 121 TCCACCACTTATATCATTAACAATCTGATTGTTAGTCCGAACTATATTGAGTAGTG 180

|||||

Db 4196 TCCACCACTTATATCATTAACAATCTGATTGTTAGTCCGAACTATATTGAGTAGTG 4137

|||||

QY 181 AACCAATAGACATTAACATTAAGGATTTATGGCTAACTCTGCAATTCATATTCT 240

|||||

Db 4136 AACCAATAGACATTAACATTAAGGATTTATGGCTAACTCTGCAATTCATATTCT 4077

|||||

QY 241 CATCGCTTAATCTGGTCAATTTTACGCTCCAGAAAGAAATTCGCAATTCCTTGACAAAT 300

|||||

Db 4076 CATCGCTTAATCTGGTCAATTTTACGCTCCAGAAAGAAATTCGCAATTCCTTGACAAAT 4017

|||||

QY 301 GTTGGCACTGGAACCTGTGCTATGTTTTACATCTCTATTAACTAGGCAAGGAGTAGAT 360

|||||

Db 4016 GTTGGCACTGGAACCTGTGCTATGTTTTACATCTCTATTAACTAGGCAAGGAGTAGAT 3957

|||||

QY 361 TATTATGACAGGAGAAATCTCTTCAGATCCCTTCCACATCAATATGTCGTAAGAACAG 420

|||||

Db 3956 TATTATGACAGGAGAAATCTCTTCAGATCCCTTCCACATCAATATGTCGTAAGAACAG 3897

|||||

QY 421 ATACAGTCTAGTGTAGTTTCTAATGACGCTCAATGCCATTTCTCTGAAGCATCTTCAG 480

|||||

Db 3896 ATACAGTCTAGTGTAGTTTCTAATGAGCGGTCAATGCCATTTCTCTGAAAGGCATGTTCTAG 3837

QY 481 AGATGATGATTTCTGGGATCCCTTGGAGGGGCCCTGAAATTCGGAACACAGTTAGTTGAGTT 540

|||||

Db 3836 AGATGATGATTTCTGGGATCCCTTGGAGGGGCCCTGAAATTCGGAACACAGTTAGTTGAGTT 3777

|||||

QY 541 TTAGTACCTTAATGCTTCTGGTTATATCTAGTGAATGCCATTTCTGTAAGCTGAGTTTC 600

|||||

Db 3776 TTAGTACCTTAATGCTTCTGGTTATATCTAGTGAATGCCATTTCTGTAAGCTGAGTTTC 3717

|||||

QY 601 TACCATCTCCACAGGAATAAAGCTTAATACCTGTCCAAAGAGTGGTGGCGCATTTGACCAA 660

|||||

Db 3716 TACCATCTCCACAGGAATAAAGCTTAATACCTGTCCAAAGAGTGGTGGCGCATTTGACCAA 3657

|||||

QY 661 ATGAAGATCACAAGCATGGCAAGATGCAATCTGGCAAGAGCCGGAATTTATTTGTAT 720

|||||

Db 3656 ATGAAGATCACAAGCATGGCAAGATGCAATCTGGCAAGAGCCGGAATTTATTTGTAT 3597

|||||

QY 721 TCTACTTACATCGAACAGGACCATATCAATGTTGCCCCAGCAGGACCCCGCAGATAAG 780

|||||

Db 3596 TCTACTTACATCGAACAGGACCATATCAATGTTGCCCCAGCAGGACCCCGCAGATAAG 3537

|||||

QY 781 TTCTGTTTCTCCACAGCAGAAATATCCCAACTGCATAGCTCCCAACAATGAATCCAA 840

|||||

Db 3536 TTCTGTTTCTCCACAGCAGAAATATCCCAACTGCATAGCTCCCAACAATGAATCCAA 3477

|||||

QY 841 ACCACATCGGCTCAGAGAGAGCTTATGATAAAGGCACTAATCTGTAATAATTTCTCTAGA 900

|||||

Db 3476 ACCACATCGGCTCAGAGAGAGCTTATGATAAAGGCACTAATCTGTAATAATTTCTCTAGA 3417

|||||

QY 901 AAGCGAATAATTAATAGCACACCTTGACCTCCACCAAGAGCTTGTGGATCGACTTTGTGCC 960

|||||

Db 3416 AAGCGAATAATTAATAGCACACCTTGACCTCCACCAAGAGCTTGTGGATCGACTTTGTGCC 3357

|||||

QY 961 CATGAAATGGCAATCTGACATCTGGTGCACCTGTCAGATCTCTCGGAAATGAGGAGCA 1020

|||||

Db 3356 CATGAAATGGCAATCTGACATCTGGTGCACCTGTCAGATCTCTCGGAAATGAGGAGCA 3297

|||||

QY 1021 TAGCTTCGCTGTGTATGTTGTGGGATATTACGCTGCTAAAACCTTTGTGTTCTGATCG 1080

|||||

Db 3296 TAGCTTCGCTGTGTATGTTGTGGGATATTACGCTGCTAAAACCTTTGTGTTCTGATCG 3237

|||||

QY 1081 ATCTGGTTAGAGAGCATCGCTTTATAGCACTTAAATGGTAGTATATCTCTCAAGG 1140

|||||

Db 3236 ATCTGGTTAGAGAGCATCGCTTTATAGCACTTAAATGGTAGTATATCTCTCAAGG 3177

|||||

QY 1141 AGCCTATACCTGCAAGAAAGGATAGCTTGGCCTGTGGGATTTGAGCCGTTGAAGGAAAC 1200

|||||

Db 3176 AGCCTATACCTGCAAGAAAGGATAGCTTGGCCTGTGGGATTTGAGCCGTTGAAGGAAAC 3117

|||||

QY 1201 AACCAATACAGTTACCTTACCAGATGTTGCCACGACATGGGCAAGCTATGCTAGAC 1260

|||||

Db 3116 AACCAATACAGTTACCTTACCAGATGTTGCCACGACATGGGCAAGCTATGCTAGAC 3057

|||||

QY 1261 CAAGAAGCAAGCAAGAAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTTCCAGAAAT 1320

|||||

Db 3056 CAAGAAGCAAGCAAGAAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTTCCAGAAAT 2997

|||||

QY 1321 ATGTTCTATCTCAGCCAGACCAATGGGGGCAAAATTTACTACTATTTGGCCATACATTAC 1380

|||||

Db 2996 ATGTTCTATCTCAGCCAGACCAATGGGGGCAAAATTTACTACTATTTGGCCATACATTAC 2937

|||||

QY 1381 CAGCTAAAAGTCTTACTCAACCTTAACCTGTTGAACGGTCTCTGTCGGCAACGGTGAG 1440

|||||

Db 2936 CAGCTAAAAGTCTTACTCAACCTTAACCTGTTGAACGGTCTCTGTCGGCAACGGTGAG 2877

|||||

QY 1441 AATGCACTTAATGAGCGGAGCAACACTTCTTTCACCGTGTCTGCTTACATCTCTGTAGAC 1500

|||||

Db 2876 AATGCACTTAATGAGCGGAGCAACACTTCTTTCACCGTGTCTGCTTACATCTCTGTAGAC 2817

|||||

QY 1501 GGTGACCGGTGAGTGTCTTCCGCATGACCGCTTGTGTTGTCGACCTCTGCGAC 1560

|||||

Db 2816 GGTGACCGGTGAGTGTCTTCCGCATGACCGCTTGTGTTGTCGACCTCTGCGAC 2757

|||||



CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
STREET: 8110 Gatehouse Road, Suite 500 East  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 2046  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/351,413  
FILING DATE:  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/899,072  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/970,849  
FILING DATE: 03-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-102PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2407 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Oryza sativa  
STRAIN: Akihikari  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..2263 /label= PEL  
OTHER INFORMATION: /note= "sequence comprising another specific  
OTHER INFORMATION: /note= "promoter PEL"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2181..2187  
OTHER INFORMATION: /label= TATA  
OTHER INFORMATION: /note= "TATA Box"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2211  
OTHER INFORMATION: /note= "transcription initiation  
OTHER INFORMATION: /note= "site determined by primer extension"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2264..2266  
OTHER INFORMATION: /label= ATG  
OTHER INFORMATION: /note= "ATG start of translation of E1 gene"  
US-08-351-413-9

```

RESULT 4
US-08-351-413-9
; Sequence 9, Application US/08351413
; Patent No. 5750867
; GENERAL INFORMATION:
; APPLICANT: Williams, Mark
; APPLICANT: Leemans, Jan
; TITLE OF INVENTION: Maintenance of male-sterile plants
; NUMBER OF SEQUENCES: 17
US-08-351-413-9
Query Match          99.9%; Score 1693.4; DB 1; Length 2407;
Best Local Similarity 99.9%; Pred. NO. 0;
Matches 1694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCAGATCCTTCTGTGTTGTTTATTAAAAATTAAATTTATTCGGAATACCTACC 60
    ||| |||||
Db   572 CCTCAGATCCTTCTGTGTTGTTTATTAAAAATTAAATTTATTCGGAATACCTACC 631

```

QY 61 AATATATAGTACTTGTCAAGCTGCAAGAACTTCCAATCGCGACAATACCAATAGAGA 120  
|||||  
Db 632 AATATATAGTAGACTTGTCAAGCTGCAAGAACTTCCAATCGCGACAATACCAATAGAGA 691  
QY 121 TCCACACACCTTATATATCATTAACAATCTGATTTAGTCCAGAACTATATAGAGTAGTG 180  
|||||  
Db 692 TCCAAACACCTTATATATCATTAACAATCTGATTTAGTCCAGAACTATATAGAGTAGTG 751  
QY 181 AACAAATAGCAGATTAACATTTATAGAGATTTATGGCTAACTCTGCAATTCATATTTCT 240  
|||||  
Db 752 AACAAATAGCAGATTAACATTTATAGAGATTTATGGCTAACTCTGCAATTCATATTTCT 811  
QY 241 GATGGCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAAATTCGCAATCTCTGGACAAT 300  
|||||  
Db 812 GATGGCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAAATTCGCAATCTCTGGACAAT 871  
QY 301 GTTGGCACTGGAACCTGTTGGATGTTTTTACATCTCTTATTAACTAGCAAAAGGAGTAGAT 360  
|||||  
Db 872 GTTGGCACTGGAACCTGTTGGATGTTTTTACATCTCTTATTAACTAGCAAAAGGAGTAGAT 931  
QY 361 TATTATGTACCAGAGAAATCTCTTCAGATCTTTCCAGATGCAATGTGCTGAAGAACAG 420  
|||||  
Db 932 TATTATGTACCAGAGAAATCTCTTCAGATCTTTCCAGATGCAATGTGCTGAAGAACAG 991  
QY 421 ATACAGTGTAGTGTAGTTTGTAAATGGACGGTCAATGCCATTTCTCTGAAGGCACTGTTTCAG 480  
|||||  
Db 992 ATACAGTGTAGTGTAGTTTGTAAATGGACGGTCAATGCCATTTCTCTGAAGGCACTGTTTCAG 1051  
QY 481 AGATGATGATTTTCGGATGCTTTGGAGGGCCCTGAAATTCGGAACAGTAGTTAGTTGAGTT 540  
|||||  
Db 1052 AGATGATGATTTTCGGATGCTTTGGAGGGCCCTGAAATTCGGAACAGTAGTTAGTTGAGTT 1111  
QY 541 TTAGTACCTAATGTCCTTGGCTTATACCTAGCTGAAATGCCATTTCTGTAAGCTGAGTTTTC 600  
|||||  
Db 1112 TTAGTACCTAATGTCCTTGGCTTATACCTAGCTGAAATGCCATTTCTGTAAGCTGAGTTTTC 1171  
QY 601 TACCATCTCCACAGGAATTAAGCTATATACCTGTCCAAAGTGGTGGCGCATTTTGACCAA 660  
|||||  
Db 1172 TACCATCTCCACAGGAATTAAGCTATATACCTGTCCAAAGTGGTGGCGCATTTTGACCAA 1231  
QY 661 ATGAAGATCACAAGCATGGCAAGAAATGGCAATCTGGCAAGGAGCGGAATTAATTTGAT 720  
|||||  
Db 1232 ATGAAGATCACAAGCATGGCAAGAAATGGCAATCTGGCAAGGAGCGGAATTAATTTGAT 1291  
QY 721 TCTACTAGATCGAACAGAACCATATCAATGTGTCGCCAGCAAGGACCCCGCAGATAAG 780  
|||||  
Db 1292 TCTACTAGATCGAACAGAACCATATCAATGTGTCGCCAGCAAGGACCCCGCAGATAAG 1351  
QY 781 TTCTGTGTTCTTCCACAGCAGATATCGCAACTGCAATAGCTCCCAACCAATGAATPCCAAA 840  
|||||  
Db 1352 TTCTGTGTTCTTCCACAGCAGATATCGCAACTGCAATAGCTCCCAACCAATGAATPCCAAA 1411  
QY 841 ACCACATCGGCTCAGAGAGAGTTATGATATAAAGGCACCTAAATCTGGAATAATTCCTAGA 900  
|||||  
Db 1412 ACCACATCGGCTCAGAGAGAGTTATGATATAAAGGCACCTAAATCTGGAATAATTCCTAGA 1471  
QY 901 AAGCAATTAATATAGCACACCTTTGACCTCCACCAAGAGCTTGGATCGACTGTGTCG 960  
|||||  
Db 1472 AAGCAATTAATATAGCACACCTTTGACCTCCACCAAGAGCTTGGATCGACTGTGTCG 1531  
QY 961 CATGAATGGCATTTCTGACATTTCTGGTCACTGTGCAAGATCTCTCGGAATAATGAGAGGCA 1020  
|||||  
Db 1532 CATGAATGGCATTTCTGACATTTCTGGTCACTGTGCAAGATCTCTCGGAATAATGAGAGGCA 1591  
QY 1021 TAGCTTGTGTGTATGTGTGTGGATATTACGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080  
|||||  
Db 1592 TAGCTTGTGTGTATGTGTGTGGATATTACGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1651  
QY 1081 ATCTGGTTAGAGACATCGCTCTTTATAAGCACTTAAAAATGGTAGTATAATCTCTCAAGG 1140  
|||||  
Db 1652 ATCTGGTTAGAGACATCGCTCTTTATAAGCACTTAAAAATGGTAGTATAATCTCTCAAGG 1711  
QY\* 1141 AGCCTATACTGCCAAGGAAGGATACCTTGGCTGTGGGATTTGAGCGCTTGAAGGGAAC 1200

Db 1712 AGCCTATACTGCCAAGGAAGGATAGCTTGGCTGTGGGATTTGAGCGCTTGAAGGGAAC 1771  
|||||  
QY 1201 AAACCAATACAGTTACCTTACCAGATGTTTGGCAACGATGGCAACGTCATTTGCTAGAC 1260  
|||||  
Db 1772 AAACCAATACAGTTACCTTACCAGATGTTTGGCAACGATGGCAACGTCATTTGCTAGAC 1831  
|||||  
QY 1261 CAAGAAGCAAGAAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTTTCCAGAAT 1320  
|||||  
Db 1832 CAAGAAGCAAGAAAGTTAGCTGTCAAAAAGATATGCTAGAGGCTTTTCCAGAAT 1891  
|||||  
QY 1321 ATGTTCTATCTCAGCAGCAACCAATGGGGCAAAATTTTACTATTTGCCATACATTAAC 1380  
|||||  
Db 1892 ATGTTCTATCTCAGCAGCAACCAATGGGGCAAAATTTTACTATTTGCCATACATTAAC 1951  
|||||  
QY 1381 CACGTAAGAAGTCTACACTCAACCTAACTGTTGAACGGTCTCTTCTGGCCAAACGGTGAG 1440  
|||||  
Db 1952 CACGTAAGAAGTCTACACTCAACCTAACTGTTGAACGGTCTCTTCTGGCCAAACGGTGAG 2011  
|||||  
QY 1441 AATGACCTAATGGACGGGACAACACTTCTTACCGTGTCTACTGTACTGTACTGTAGAC 1500  
|||||  
Db 2012 AATGACCTAATGGACGGGACAACACTTCTTACCGTGTCTACTGTACTGTACTGTAGAC 2071  
|||||  
QY 1501 GSTGACGCGTGAGTGCTTTTGGCATGACCGTCTTGGTGTGGCAGTCACCTTGGCGCAC 1560  
|||||  
Db 2072 GSTGACGCGTGAGTGCTTTTGGCATGACCGTCTTGGTGTGGCAGTCACCTTGGCGCAC 2131  
|||||  
QY 1561 GCTTGCACGGTGACHTCACCTGCGCATTTGCCCGCGCTGCGCGCGCTTACAAAAGCCA 1620  
|||||  
Db 2132 GCTTGCACGGTGACHTCACCTGCGCATTTGCCCGCGCTGCGCGCGCTTACAAAAGCCA 2191  
|||||  
QY 1621 CACAGCAGCGCGGCGGACGATTAACCATCTCTAGCATCCCGGTGTCAGCAAGAGATCCAT 1680  
|||||  
Db 2192 CACAGCAGCGCGGCGGACGATTAACCATCTCTAGCATCCCGGTGTCAGCAAGAGATCCAT 2251  
|||||  
QY 1681 CAAGCGTTCGCGATG 1695  
|||||  
Db 2252 CAAGCGTTCGCGATG 2266  
|||||

## RESULT 5

US-09-025-583-9  
; Sequence 9, Application US/09025583  
; Patent No. 5977433  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Mark  
; APPLICANT: Leemans, Jan  
; TITLE OF INVENTION: Maintenance of male-sterile plants  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH  
; STREET: 8110 Gatehouse Road, Suite 500 East  
; CITY: Falls Church  
; STATE: Virginia  
; COUNTRY: U.S.A.  
; ZIP: 2046  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/025,583  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/351,413  
; FILING DATE:  
; APPLICATION NUMBER: US 07/899,072  
; FILING DATE: 12-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/970,849  
; FILING DATE: 03-NOV-1992

ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30,330  
REFERENCE/DOCKET NUMBER: 2121-102PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2407 base pairs  
TYPE: nucleic acid  
STRAINEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Oryza sativa  
STRAIN: Akhikari  
FEATURE:

NAME/KEY: -  
LOCATION: 1..2263  
OTHER INFORMATION: /label= PE1  
OTHER INFORMATION: /note= "sequence comprising another specific  
OTHER INFORMATION: promoter PE1"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2181..2187  
OTHER INFORMATION: /label= TATA  
OTHER INFORMATION: /note= "TATA Box"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2211  
OTHER INFORMATION: /note= "transcription initiation  
OTHER INFORMATION: site determined by primer extension"  
FEATURE:  
NAME/KEY: -  
LOCATION: 2264..2266  
OTHER INFORMATION: /label= ATG  
OTHER INFORMATION: /note= "ATG start of translation of El gene"  
US-09-025-583-9

Query Match 99.9%; Score 1693.4; DB 2; Length 2407;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCGCAGATCCCTCTGCTGATGTTTATTTAAATTTTATCTGGAATACCTACC 60  
Db 572 CCTCAGATCCCTCTGCTGATGTTTATTTAAATTTTATCTGGAATACCTACC 631  
Qy 61 AATATATAGTAGACTTGCTCAAGCTGCAAGAACTTCCAATCGCGACAAATACCAATAGAGA 120  
Db 632 AATATATAGTAGACTTGCTCAAGCTGCAAGAACTTCCAATCGCGACAAATACCAATAGAGA 691  
Qy 121 TCCAAACCACCTTAAATATCAATCAATCTGATGTTAGTCCAGAACTATATTGAGTAGTG 180  
Db 692 TCCAAACCACCTTAAATATCAATCAATCTGATGTTAGTCCAGAACTATATTGAGTAGTG 751  
Qy 181 AACAAACATAGCACATTAACATTTATGAGGATTTATTTGGCTAACTCTGCAATTCATATTTCT 240  
Db 752 AACAAACATAGCACATTAACATTTATGAGGATTTATTTGGCTAACTCTGCAATTCATATTTCT 811  
Qy 241 GATCGGCTTAATCTGCTCAATTTAGCGCTCCAGAAAGAAATTCACAACTCTTGGACAAT 300  
Db 812 GATCGGCTTAATCTGCTCAATTTAGCGCTCCAGAAAGAAATTCACAACTCTTGGACAAT 871  
Qy 301 GTTGGCACTGGAAGTGTGATGTTTTTATCTCTTATTAACGTAGCAAGAGTAGTAG 360  
Db 872 GTTGGCACTGGAAGTGTGATGTTTTTATCTCTTATTAACGTAGCAAGAGTAGTAG 931  
Qy 361 TATTATGTACCAGAGAAATCTCTTCAGATCCTTTCCACATGCAATGTCTGAAGACACAG 420  
|||||

Db 932 TATTATGTACCAGAGAAATCTCTTCAGATCCTTTCCACATGCAATGCTCGTAAGACACAG 991  
Qy 421 ATACAGTGTACGTTAGTTGTAATGAGCGGTCAATGCCATTTCTCTGAAGCATGTTTCAG 480  
|||||  
Db 992 ATACAGTGTACGTTAGTTGTAATGAGCGGTCAATGCCATTTCTCTGAAGCATGTTTCAG 1051  
|||||  
Qy 481 AGATGATGATTTCTGGATCCTTTGGAGGGCCCTGAAATTCGGAACAGTTAGTTGAGTT 540  
|||||  
Db 1052 AGATGATGATTTCTGGATCCTTTGGAGGGCCCTGAAATTCGGAACAGTTAGTTGAGTT 1111  
|||||  
Qy 541 TTAGTACCTTAATGTTGCTTATCTACTAGTGAATGCCATTTCTCTGAAGCATGTTTC 600  
|||||  
Db 1112 TTAGTACCTTAATGTTGCTTATCTACTAGTGAATGCCATTTCTCTGAAGCATGTTTC 1171  
|||||  
Qy 601 TACCATCTCCACAGAGAAATAAAGCTAATACCTGTCTCAAGAGTGTGGGCAATTTGACCAA 660  
|||||  
Db 1172 TACCATCTCCACAGAGAAATAAAGCTAATACCTGTCTCAAGAGTGTGGGCAATTTGACCAA 1231  
|||||  
Qy 661 ATGAAGATCAAGCATGCGCAAGATGCAATCTGCAAGAGGCGGAATATATATGCTAT 720  
|||||  
Db 1232 ATGAAGATCAAGCATGCGCAAGATGCAATCTGCAAGAGGCGGAATATATATGCTAT 1291  
|||||  
Qy 721 TCTACTACATCGAAGAGAACCATATCAATGTTGCCAGCAAGACCCCGCAGATAAG 780  
|||||  
Db 1292 TCTACTACATCGAAGAGAACCATATCAATGTTGCCAGCAAGACCCCGCAGATAAG 1351  
|||||  
Qy 781 TTCTCTGTTCTTCCACAGCAGATATCCGCAACTGATAGCTCCCAACAATGAAATCCAAA 840  
|||||  
Db 1352 TTCTCTGTTCTTCCACAGCAGATATCCGCAACTGATAGCTCCCAACAATGAAATCCAAA 1411  
|||||  
Qy 841 ACCACATCGGCTCAGAGAGAGTTATGATAAAGGCACTAATCTGTAATATTTCTTAGA 900  
|||||  
Db 1412 ACCACATCGGCTCAGAGAGAGTTATGATAAAGGCACTAATCTGTAATATTTCTTAGA 1471  
|||||  
Qy 901 AAGGGAATAATAATAGCACACCTTGACCTCCCAAGAGCTTGTGGATGCACTGTGGCC 960  
|||||  
Db 1472 AAGGGAATAATAATAGCACACCTTGACCTCCCAAGAGCTTGTGGATGCACTGTGGCC 1531  
|||||  
Qy 961 CATGAAATGCGATCTGACATCTGGTCACTGTCAGATCTCTCGGAAATGAGGAGCA 1020  
|||||  
Db 1532 CATGAAATGCGATCTGACATCTGGTCACTGTCAGATCTCTCGGAAATGAGGAGCA 1591  
|||||  
Qy 1021 TAGCTTCGCTGTGTATGTGTGGGATATTACGCTGCTAAAACCTTTCTGTTCTGATCG 1080  
|||||  
Db 1592 TAGCTTCGCTGTGTATGTGTGGGATATTACGCTGCTAAAACCTTTCTGTTCTGATCG 1651  
|||||  
Qy 1081 ATCTGTTAGAGAGATCGTCTTTATAAGCACTTAAAATGCTAGTATAATCTCTCAAGG 1140  
|||||  
Db 1652 ATCTGTTAGAGAGATCGTCTTTATAAGCACTTAAAATGCTAGTATAATCTCTCAAGG 1711  
|||||  
Qy 1141 AGCCTATACCTCCCAAGSAAAGGATAGCTTTGGCCTGTGGGGATTTGAGCGGTTGAAGGGAAC 1200  
|||||  
Db 1712 AGCCTATACCTCCCAAGSAAAGGATAGCTTTGGCCTGTGGGGATTTGAGCGGTTGAAGGGAAC 1771  
|||||  
Qy 1201 AAAGCAATACAGTTACCTTACAGATGTTTCCACGACATGGCAACGTCATTCCTAGAC 1260  
|||||  
Db 1772 AAAGCAATACAGTTACCTTACAGATGTTTCCACGACATGGCAACGTCATTCCTAGAC 1831  
|||||  
Qy 1261 CAAGAAGCAAGSAAAGGTTTGTAGCTGTCAAAAAGATATGCTAGAGGCTTTCCAGAAAT 1320  
|||||  
Db 1832 CAAGAAGCAAGSAAAGGTTTGTAGCTGTCAAAAAGATATGCTAGAGGCTTTCCAGAAAT 1891  
|||||  
Qy 1321 ATGTTCTATCTCAGCAGACCAATGGGCAAAATTTACTACTATTTGCCATACATTAAC 1380  
|||||  
Db 1892 ATGTTCTATCTCAGCAGACCAATGGGCAAAATTTACTACTATTTGCCATACATTAAC 1951  
|||||  
Qy 1381 CACGTAAAGTCTTACACTCAACCTAACTGTTTGAAGGCTCTGTTCTGGCCAAACGGTAG 1440  
|||||  
Db 1952 CACGTAAAGTCTTACACTCAACCTAACTGTTTGAAGGCTCTGTTCTGGCCAAACGGTAG 2011  
|||||  
Qy 1441 AATGCACTTAATGAGGGGACAACTCTTTTCCGCTGCTACTCTACATCCTGCTAGAC 1500  
|||||  
Db 2012 AATGCACTTAATGAGGGGACAACTCTTTTCCGCTGCTACTCTGCTACTGCTAGAC 2071  
|||||





QY 1081 ATCTGTTAGAGCATCGTCTTTATAGCACTTAAATGCTAGTATATCTCTCAAGG 1140  
|||||  
Db 3236 ATCTGTTAGAGCATCGTCTTTATAGCACTTAAATGCTAGTATATCTCTCAAGG 3177  
|||||  
QY 1141 AGCTATATCTGCAAGCAAGAGTAGCTTGGCTCTGGGGATTGAGCGTTGAAGGAAC 1200  
|||||  
Db 3176 AGCTATATCTGCAAGCAAGAGTAGCTTGGCTCTGGGGATTGAGCGTTGAAGGAAC 3117  
|||||  
QY 1201 AAACGAATACAGTTACCTTACACAGATGTTTGGCAGCATGGCAAGTCAATGCTAGAC 1260  
|||||  
Db 3116 AAACGAATACAGTTACCTTACACAGATGTTTGGCAGCATGGCAAGTCAATGCTAGAC 3057  
|||||  
QY 1261 CAAGAAGCAAGAAAGCAAGCTTTAGCTGTCAAAAGAGATATGCTAGAGGCTTTCCAGAA 1320  
|||||  
Db 3056 CAAGAAGCAAGAAAGCAAGCTTTAGCTGTCAAAAGAGATATGCTAGAGGCTTTCCAGAA 2997  
|||||  
QY 1321 ATGTTCTATCTACGACAGACCAATGGGGGCAAAATTTTACTACTATTTGGCCATACATTAAC 1380  
|||||  
Db 2996 ATGTTCTATCTACGACAGACCAATGGGGGCAAAATTTTACTACTATTTGGCCATACATTAAC 2937  
|||||  
QY 1381 CAGGTAAAGTCTTACACTCAACTTAACCTGTTGAACGGTCTCTGTCGCAACGGTGAG 1440  
|||||  
Db 2936 CAGGTAAAGTCTTACACTCAACTTAACCTGTTGAACGGTCTCTGTCGCAACGGTGAG 2877  
|||||  
QY 1441 ATGCACTTAATGACGGGACACACTCTTTCACCGTCTACTGCTACATCTCTGTAGAC 1500  
|||||  
Db 2876 ATGCACTTAATGACGGGACACACTCTTTCACCGTCTACTGCTACATCTCTGTAGAC 2817  
|||||  
QY 1501 GGTGACCGGTGAGGTCTTTTCGCCATGACCGTCTCTGTTGTTGSCAGTCACTTGGCGAC 1560  
|||||  
Db 2816 GGTGACCGGTGAGGTCTTTTCGCCATGACCGTCTCTGTTGTTGSCAGTCACTTGGCGAC 2757  
|||||  
QY 1561 GCTTCACCGTGACTCACTGCCACATTCGCCCGCTGCGCGCGCTACAAAAGCCA 1620  
|||||  
Db 2756 GCTTCACCGTGACTCACTGCCACATTCGCCCGCTGCGCGCGCTACAAAAGCCA 2697  
|||||  
QY 1621 CACAGCACGGCGGCCACAGATACCATCTAGCATCCCGGTGTCAGCAAGAGATCCAT 1680  
|||||  
Db 2696 CACAGCACGGCGGCCACAGATACCATCTAGCATCCCGGTGTCAGCAAGAGATCCAT 2637  
|||||  
QY 1681 CAAGCGCTCGGATG 1695  
|||||  
Db 2636 CAAGCGCTCGATG 2622  
|||||

## RESULT 7

US-09-458-093-1/c  
; Sequence 1, Application US/09458093  
; Patent No. 6344602  
; GENERAL INFORMATION:  
; APPLICANT: PLANT GENETIC SYSTEMS N.V.  
; TITLE OF INVENTION: Method to obtain male sterile plants  
; FILE REFERENCE: NMSCOR  
; CURRENT APPLICATION NUMBER: US/09/458,093  
; PRIOR FILING DATE: 1999-12-10  
; PRIOR APPLICATION NUMBER: 08/894,440  
; PRIOR FILING DATE: 1997-11-12  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 6548  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pTSL74  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(2003)  
; OTHER INFORMATION: pUC19 derived vector sequences (vector)  
; NAME/KEY: misc\_feature  
; LOCATION: Complement((2019)..(2283))  
; OTHER INFORMATION: 3' nos: region containing polyadenylation signal  
; OTHER INFORMATION: of nopaline synthase gene of Agrobacterium

; NAME/KEY: misc\_feature  
; LOCATION: Complement((2284)..(2624))  
; OTHER INFORMATION: region coding for barnase of Bacillus  
; OTHER INFORMATION: amylioliquefaciens  
; NAME/KEY: misc\_feature  
; LOCATION: Complement((2625)..(4313))  
; OTHER INFORMATION: promoter of the stamen-specific E1 gene of rice  
; OTHER INFORMATION: (PE1)  
; NAME/KEY: misc\_feature  
; LOCATION: (4336)..(5710)  
; OTHER INFORMATION: 35S promoter of Cauliflower Mosaic Virus (P35S)  
; NAME/KEY: misc\_feature  
; LOCATION: (5711)..(6262)  
; OTHER INFORMATION: region coding for phosphinothricin acetyl  
; OTHER INFORMATION: transferase (bar)  
; NAME/KEY: misc\_feature  
; LOCATION: (6263)..(6496)  
; OTHER INFORMATION: region containing polyadenylation signal fo gene 7  
; OTHER INFORMATION: of Agrobacterium T-DNA (3'97)  
US-09-458-093-1

Query Match 99.9%; Score 1693.4; DB 4; Length 6548;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1694; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGCAGATCCCTCTGCTGATGCTTTTATTAATAATTTAATATTTATCGGAATACCTACC 60  
|||||  
Db 4316 CCGCAGATCCCTCTGCTGATGCTTTTATTAATAATTTAATATTTATCGGAATACCTACC 4257  
|||||  
QY 61 AATATATAGTAGACTTGTCAAGCTGCCAAGAACTTCAATCGCGGACAAATACCAATAGAGA 120  
|||||  
Db 4256 AATATATAGTAGACTTGTCAAGCTGCCAAGAACTTCAATCGCGGACAAATACCAATAGAGA 4197  
|||||  
QY 121 TCCACCACTTATATATCATAAACAATCTGATTTAGTCCAGAACTATATTTAGTAGTG 180  
|||||  
Db 4196 TCCACCACTTATATATCATAAACAATCTGATTTAGTCCAGAACTATATTTAGTAGTG 4137  
|||||  
QY 181 AACACAATAGCAGATTAACATATATGAGGATTTATGGCTAACTCTGCAATTTCAATATTTCT 240  
|||||  
Db 4136 AACACAATAGCAGATTAACATATATGAGGATTTATGGCTAACTCTGCAATTTCAATATTTCT 4077  
|||||  
QY 241 GATGGCTCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAAATTCACAAATCTCTGCAAT 300  
|||||  
Db 4076 GATGGCTCTAATCTGGTCAATTTTAGCGCTCCAGAAAGAAATTCACAAATCTCTGCAAT 4017  
|||||  
QY 301 GTTGGCACTGGAACCTGTTGCATGTTTATACATCTCTTATTAACGTAGCAAGAGTAGAT 360  
|||||  
Db 4016 GTTGGCACTGGAACCTGTTGCATGTTTATACATCTCTTATTAACGTAGCAAGAGTAGAT 3957  
|||||  
QY 361 TATTATGTACCAGGAGAAATCTCTTCAGATCCCTTTCCACATGCAATGTCGTAAGAAGACAG 420  
|||||  
Db 3956 TATTATGTACCAGGAGAAATCTCTTCAGATCCCTTTCCACATGCAATGTCGTAAGAAGACAG 3897  
|||||  
QY 421 ATACAGTCTACCTTAGTTTGTAAATGGACGCTCAATGCCATTTCTCTGAAGCATGTTTCAG 480  
|||||  
Db 3896 ATACAGTCTACCTTAGTTTGTAAATGGACGCTCAATGCCATTTCTCTGAAGCATGTTTCAG 3837  
|||||  
QY 481 AGATGATGATTTCTGGGATCCCTTGGAGGGCCCTGAAATTCGGAACAGTATTAGTTGATTT 540  
|||||  
Db 3836 AGATGATGATTTCTGGGATCCCTTGGAGGGCCCTGAAATTCGGAACAGTATTAGTTGATTT 3777  
|||||  
QY 541 TTAGTACCTTAATGTTCTTGCCTTATACGTAAATGCCATTTCTGTAAGCTGAGTTTTC 600  
|||||  
Db 3776 TTAGTACCTTAATGTTCTTGCCTTATACGTAAATGCCATTTCTGTAAGCTGAGTTTTC 3717  
|||||  
QY 601 TACCATCTCCACAGGAATAAAGCTAATACCTGTCCAAGAGTGGTGGCGCATTTTGACCAA 660  
|||||  
Db 3716 TACCATCTCCACAGGAATAAAGCTAATACCTGTCCAAGAGTGGTGGCGCATTTTGACCAA 3657  
|||||  
QY 661 ATGAAGATCACAAGCATGGCAAGAAATGGCAATCTGGCAAGGAGCGGAATATATTTGAT 720  
|||||  
Db 3656 ATGAAGATCACAAGCATGGCAAGAAATGGCAATCTGGCAAGGAGCGGAATATATTTGAT 3597  
|||||

```
QY 721 TCTACTACATCGAAGCAAGCATATCAATGTTGCCCGCAGAGGACCCCGCAGATAAG 780
DB 3596 TCTACTACATCGAAGCAAGCATATCAATGTTGCCCGCAGAGGACCCCGCAGATAAG 3537
QY 781 TTCTGTTCTTCCACAGCAGAAATATCCGCACTGCTAGCTCCCAACATGAATCCAAA 840
DB 3536 TTCTGTTCTTCCACAGCAGAAATATCCGCACTGCTAGCTCCCAACATGAATCCAAA 3477
QY 841 ACCACATCGCGCTCAGAGAGAACTATATGATNAAGGCACTAAATTTCTGAATPAATTTCTCTAGA 900
DB 3476 ACCACATCGCGCTCAGAGAGAACTATATGATNAAGGCACTAAATTTCTGAATPAATTTCTCTAGA 3417
QY 901 AAGGCAATATATAGCACACCTTGACCTCCACCAAGCACTGTTGATGCTGACCTGTCGC 960
DB 3416 AAGGCAATATATAGCACACCTTGACCTCCACCAAGCACTGTTGATGCTGACCTGTCGC 3357
QY 961 CATGAATGCAATTCGACATTCCTGGTCACCTGCTCAGAACTCTTCGGAATAAGAGAGCA 1020
DB 3356 CATGAATGCAATTCGACATTCCTGGTCACCTGCTCAGAACTCTTCGGAATAAGAGAGCA 3297
QY 1021 TAGCTTCGCTGCTGATGTTGTTGGGATATTTACGCTGCTAAAACCTTTGTTCTCTGATCG 1080
DB 3296 TAGCTTCGCTGCTGATGTTGTTGGGATATTTACGCTGCTAAAACCTTTGTTCTCTGATCG 3237
QY 1081 ATCTGGTTAGAGAGCATCTCTTTATAGCACTTAAATGCTAGTATATCTCTCAAG 1140
DB 3236 ATCTGGTTAGAGAGCATCTCTTTATAGCACTTAAATGCTAGTATATCTCTCAAG 3177
QY 1141 AGCCTATCTGCAAGGAAGATAGCTTGGCTGTGGGATTTGACCGCTTGAAGGGAAC 1200
DB 3176 AGCCTATCTGCAAGGAAGATAGCTTGGCTGTGGGATTTGACCGCTTGAAGGGAAC 3117
QY 1201 AAACGAATACAGTTACCTTTACAGATGTTTGCACACATGCGCAACGTCATGCTAGAC 1260
DB 3116 AAACGAATACAGTTACCTTTACAGATGTTTGCACACATGCGCAACGTCATGCTAGAC 3057
QY 1261 CAAGAAGCAAGCAAGTTTACCTGTCACAAAAGATATGCTAGAGCCTTCCAGAA 1320
DB 3056 CAAGAAGCAAGCAAGTTTACCTGTCACAAAAGATATGCTAGAGCCTTCCAGAA 2997
QY 1321 ATGTTCTATCTCAGCAGACCAATGGGGCAAAATTTTACTACTATTTGCCATACATTAAC 1380
DB 2996 ATGTTCTATCTCAGCAGACCAATGGGGCAAAATTTTACTACTATTTGCCATACATTAAC 2937
QY 1381 CACGTAAAGTCTCCTACCTCAACCTAACCTGTTGAACGGTCTCTCTGCCCAACGGTCAG 1440
DB 2936 CACGTAAAGTCTCCTACCTCAACCTAACCTGTTGAACGGTCTCTCTGCCCAACGGTCAG 2877
QY 1441 AATCCACCTAATGGAGCGGACCAACTCTTTTACCGTGTACTGTCTACATCTCTGATAG 1500
DB 2876 AATCCACCTAATGGAGCGGACCAACTCTTTTACCGTGTACTGTCTACATCTCTGATAG 2817
QY 1501 GGTGGACCGGTGAGGTGCTTTTCCGCAATGACCGTCTTGGTGTGTCAGTCACTTCCGCAC 1560
DB 2816 GGTGGACCGGTGAGGTGCTTTTCCGCAATGACCGTCTTGGTGTGTCAGTCACTTCCGCAC 2757
QY 1561 GCTTGGACCGGTGACTCACCTGCCATGTCGCCCGCGCGTCCGCGGCGCTACAAAGCCA 1620
DB 2756 GCTTGGACCGGTGACTCACCTGCCATGTCGCCCGCGCGTCCGCGGCGCTACAAAGCCA 2697
QY 1621 CACAGCGACCGCGGACGATACCCATCTCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 1680
DB 2696 CACAGCGACCGCGGACGATACCCATCTCTAGCATCCCGGTGTCCAGCAAGAGATCCAT 2637
QY 1681 CAAGCGGTGCGGATG 1695
DB 2636 CAAGCGGTGCGGATG 2622
```

```
RESULT 8
US-09-134-001C-2341
; Sequence 2341, Application US/09134001C
; Patent No. 6380370
```

```
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2341
; LENGTH: 3033
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-2341
```

```
Query Match 2.2%; Score 37.6; DB 4; Length 3033;
Best Local Similarity 49.0%; Pred. No. 0.17;
Matches 100; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
```

```
QY 87 AAGAACTTCCAATCGCCGACAAATACCAATAGAGATCCACACCTTAATATCATAAACAA 146
DB 2403 AATAGCTACGATTAGCTATAAATAGATAATTAACCTCTAACAAATTTAATAAATAAAAA 2462
QY 147 TCTGATTGTTAGTCCGAACATATATTGATGATGACGAACAATAGCATTAAACATTATG 206
DB 2463 TATAATTACGATTCGATGATGAATTAAGTGCACAAAGAAATTTCTGCTATCAGA 2522
QY 207 AGGATTATTGGCTTAACCTCTGCAATTCAAATATTCTGATGCTCTAATCTGTCATTTAG 266
DB 2523 AATATTAGCTGGTAAAAATGATTATAAATTAACACTAGAAAAATATGTTTAAATTTATTA 2582
QY 267 CGCTCCGAGAAGAAATGCAACATC 290
DB 2583 CTTGGAAAAAATAATTTTCAAGC 2606
```

```
RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEFFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOMLPOX VIRUS
; NUMBER OF SEQUENCE: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
```

Query Match 2.1%; Score 35.6; DB 4; Length 29793;  
Best Local Similarity 50.6%; Pred. No. 3.5;  
Matches 86; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

